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Convolutional Neural Network Based Brain Tumor Classification from Mri

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Biopsies, which are typically not performed prior to definitive brain surgery, are used to classify brain tumors. Technological advancements and machine learning can assist radiologists in diagnosing tumors without the need for invasive procedures. The Convolutional Neural Network (CNN) is a machine-learning technique that has produced notable outcomes in picture segmentation and classification. We introduce a novel CNN architecture for classifying three different kinds of brain tumors. Tested using T1-weighted contrast-enhanced magnetic resonance imaging, the generated network is easier to use than pre-existing pre-trained networks. Four methods were used to assess the network's performance: two databases and combinations of two 10-fold cross-validation techniques. Subject-wise cross-validation, one of the ten-fold approaches, was used to assess the network's generalization ability, and an updated picture database was used to test the improvement. The record-wise cross-validation for the enhanced data set yielded the best result for the 10-fold cross-validation approach, with an accuracy of 96.56%. The newly created CNN architecture has the potential to be a useful decision-support tool for radiologists working in medical diagnostics because of its strong generalization ability and quick execution speed.

Keywords: CNN, Gliomas, Relu, Center for Biomedical Image Computing & Analytics (CBICA).

1. Introduction

The World Health Organization (WHO) reports that cancer is the second most common cause of death worldwide. While it's not always feasible, early cancer detection can save lives. Tumors can be benign, precancerous, or malignant, in contrast to cancer. Benign tumors are different from malignant ones in that they may be surgically removed and often do not spread to other organs and tissues. Gliomas, meningiomas, and pituitary tumors are a few examples of primary brain tumors. Tumors that originate from brain structures other than nerve cells and blood vessels are referred to as gliomas. In contrast, pituitary tumors are lumps that reside inside the skull, while meningiomas develop from the membranes that envelop the brain and the central nervous system. The most significant distinction among these three tumor forms is that gliomas are usually aggressive, whereas meningiomas are usually benign. Unlike meningiomas, which grow slowly, pituitary tumors, even if benign, can cause other medical harm. Given the foregoing knowledge, accurately distinguishing between these three tumor types is a critical step in the clinical diagnostic process and, ultimately, in the successful evaluation of patients. Magnetic Resonance Imaging (MRI) is the most widely used technique for tumor type differential diagnosis. However, a lot of data is hard for humans to observe, and it is vulnerable to human subjectivity. The radiologist's experience is mostly responsible for early brain tumor identification. Before determining whether the tumor is benign or malignant, the diagnostic process could not be finished. A biopsy is typically carried out to determine whether the tissue is benign or cancerous. The biopsy of a brain tumor is typically not performed prior to definitive brain surgery, in contrast to cancers found elsewhere in the body. The development of an efficient diagnostics tool for tumor segmentation and classification from MRI images is crucial for obtaining accurate diagnosis while avoiding surgery and subjectivity. The medical industry has been greatly impacted by the development of new technologies, particularly artificial intelligence and machine learning, which offer crucial support for many medical specialties, including imaging. To give radiologists a second view, many machine-learning techniques for picture segmentation and classification are used in MRI image processing. The Multimodal Brain Tumor Segmentation Challenge (BRATS), an online competition, has been held since 2012 by the University of Pennsylvania's Perelman School of Medicine, Center for Biomedical Image Computing & Analytics (CBICA). Following the conclusion of the competition, the image databases utilized in BRATS are made publicly available. Numerous articles describe various classification techniques created with these image databases. The databases, however, are often limited, with an average of 285 photos, and they frequently include images that indicate two tumor levels—low and high levels of glioma tumors—that were obtained in the axial plan In the literature, there are other algorithms and different modifications of the pre-trained networks that are used for image analysis, classification, and segmentation. Different approaches have been tested on other medical databases, both on MRI images of brain tumors and on tumors from different parts of the human body. These papers were not considered further, as the focus was on the papers using the same MRI image database that we used.

2. Related Works

In this section, we go over the various applications of deep learning and machine learning to the analysis of medical images and the investigation of infectious brain tumors. Medical image analysis has garnered a lot of attention and academic interest over the last 20 years due to its many applications in healthcare, especially in patient inquiry and diagnosis. Studies propose machine learning-based methods for brain image classification and brain architecture analysis [9].

An extensive analysis of the various techniques for diagnosing brain MRI scans was carried out by Abd-Ellah et al. [31], who also compared and contrasted the advantages and disadvantages of deep learning and conventional machine learning techniques. The authors also introduced a novel semi-automatic segmentation method for brain tumor images. [32]

"DeepMedic," a 3D CNN architecture for brain tumor segmentation, was introduced by Kamnitsas et al. [60]. Their model made use of fully connected conditional random fields (CRF) to incorporate contextual information and multi-scale inputs. The method outperformed earlier techniques and proved the efficacy of deep learning for precise tumor segmentation by achieving competitive performance on the BraTS 2013 and 2014 datasets. Furthermore, Liang et al. [33] developed a multi-modal fusion deep learning model for brain tumor grading. Their method combined features from MRI images and clinical data and achieved high accuracy in classifying tumor grades, demonstrating the potential of deep learning in aiding clinical decision-making.

Drawbacks

- The biggest problem with classifying and segmenting the MRI images with some neural networks lies in the number of images in the database.
- In addition, MRI images are acquired in different planes, so the option of using all the available planes could enlarge the database. As this could generally affect the classification output by overfitting, pre-processing is required before feeding the images into the neural network.
- The existing system is prone to the over-fitting problem for datasets with noisy classification/regression tasks.
- Computations are complex and time-consuming.

Development of Brain Tumor Classification from Mri using Cnn

Tumor classification was performed using a CNN (Efficient Net) developed in Python. The network architecture consists of input, two main blocks, classification block, and output, as shown in Figure 1.

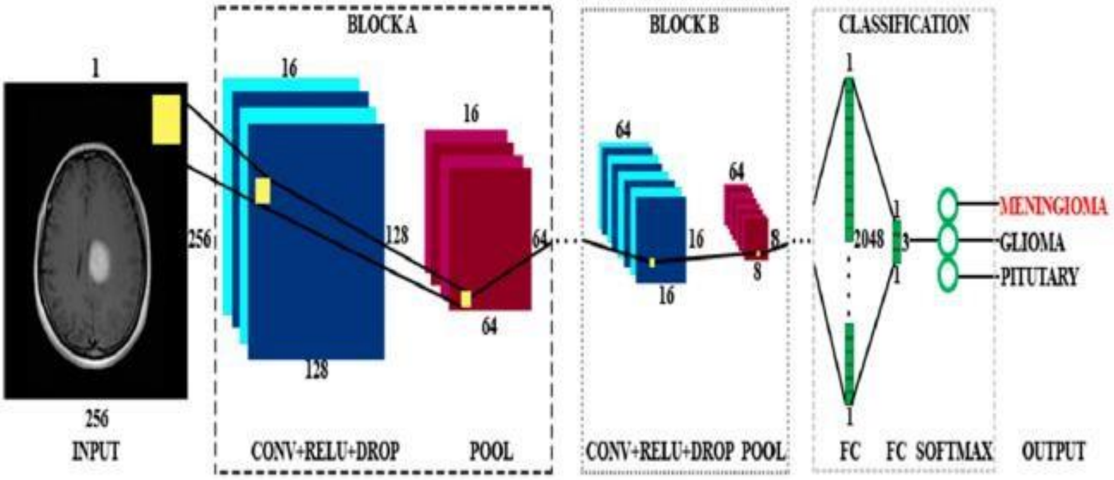
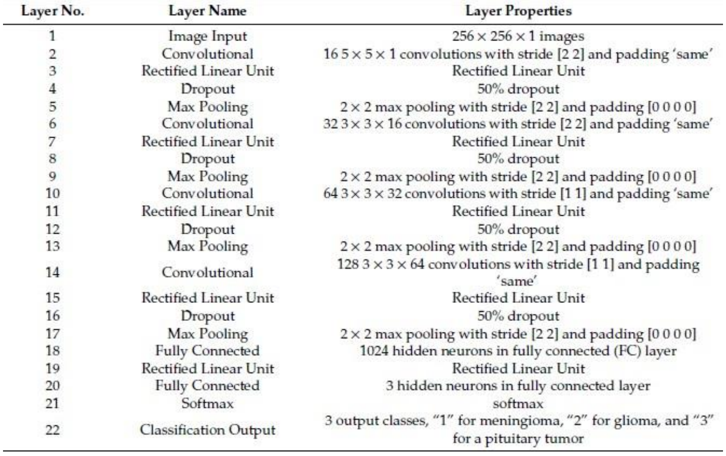


Figure 1: CNN Architecture

Figure 1: The input layer, two Blocks A and B, the classification block, and the output are all shown in this schematic illustration of a convolutional neural network (CNN) architecture. Only the convolution layer is different in Block B. Block A's convolution layer produces an output that is twice as small as the input, whereas Block B's convolutional layer produces an output that is the same size as the input.

The first main block, Block A, consists of a convolutional layer which as an output gives an image two times smaller than the provided input. The convolutional layer is followed by the Rectified Linear Unit (ReLU) activation layer and the dropout layer. In this block, there is also the max pooling layer which gives an output two times smaller than the input. The second block, Block B, is different from the first only in the convolution layer, which retains the same output size as the input size of that layer. The classification block consists of two Fully Connected (FC) layers, of which the first one represents the flattened output of the last max pooling layer, whereas, in the second FC layer, the number of hidden units is equal to the number of the classes of tumor. The whole network architecture consists of the input layer, two Blocks A, two Blocks B, classification block, and output layer; altogether, there are 22 layers, as shown in Table 1.

Table 1: New Cnn Architecture. All Network Layers are listed with their Properties



Layer No.	Layer Name	Layer Properties
1	Image Input	256 × 256 × 1 images
2	Convolutional	16 5 × 5 × 1 convolutions with stride [2 2] and padding 'same'
3	Rectified Linear Unit	Rectified Linear Unit
4	Dropout	50% dropout
5	Max Pooling	2 × 2 max pooling with stride [2 2] and padding [0 0 0 0]
6	Convolutional	32 3 × 3 × 16 convolutions with stride [2 2] and padding 'same'
7	Rectified Linear Unit	Rectified Linear Unit
8	Dropout	50% dropout
9	Max Pooling	2 × 2 max pooling with stride [2 2] and padding [0 0 0 0]
10	Convolutional	64 3 × 3 × 32 convolutions with stride [1 1] and padding 'same'
11	Rectified Linear Unit	Rectified Linear Unit
12	Dropout	50% dropout
13	Max Pooling	2 × 2 max pooling with stride [2 2] and padding [0 0 0 0]
14	Convolutional	128 3 × 3 × 64 convolutions with stride [1 1] and padding 'same'
15	Rectified Linear Unit	Rectified Linear Unit
16	Dropout	50% dropout
17	Max Pooling	2 × 2 max pooling with stride [2 2] and padding [0 0 0 0]
18	Fully Connected	1024 hidden neurons in fully connected (FC) layer
19	Rectified Linear Unit	Rectified Linear Unit
20	Fully Connected	3 hidden neurons in fully connected layer
21	Softmax	softmax
22	Classification Output	3 output classes, "1" for meningioma, "2" for glioma, and "3" for a pituitary tumor

Contributions

- The aim of this research is firstly to examine the classification of tumor types from an imbalanced database with a CNN. Although considered large compared to other available MRI image databases, this database is still far smaller than databases generally used in the field of artificial intelligence.
- We wanted to show that the performance of the small architecture could compare favorably with the performance of the more complex ones. Using a simpler network requires fewer resources for

training and implementation. This is a crucial problem to address because limited available resources make it difficult to use the system in clinical diagnostics and on mobile platforms.

- If the system is needed to be used in everyday clinical diagnostics, it should be generally applicable.

Benefits

- Compared to pre-trained networks, our neural network design is less complicated, and it can be operated on standard, contemporary personal computers. This is made achievable by the algorithm's significantly lower implementation and training resource requirements.
- The importance of developing smaller networks is also linked to the possibility of deploying the algorithm on mobile platforms, which is significant for diagnostics in developing countries.
- In addition, the network has a very good execution speed of 15 ms per image.
- A comparison with the comparable state-of-the-art methods shows that our network obtained better results. The best result for 10-fold cross-validation was achieved for the record-wise method and, for the augmented dataset, and the accuracy was 98.56%.

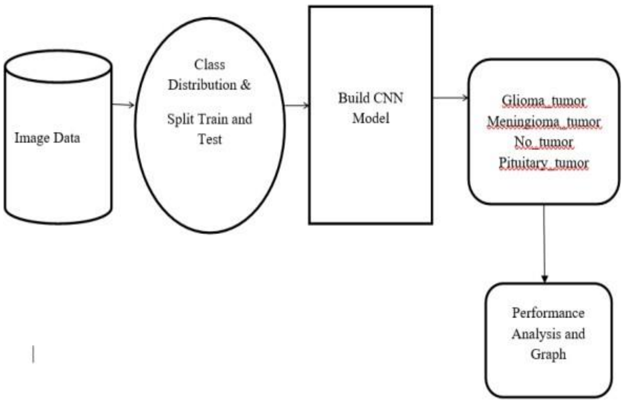


Figure 2: Flow Chart

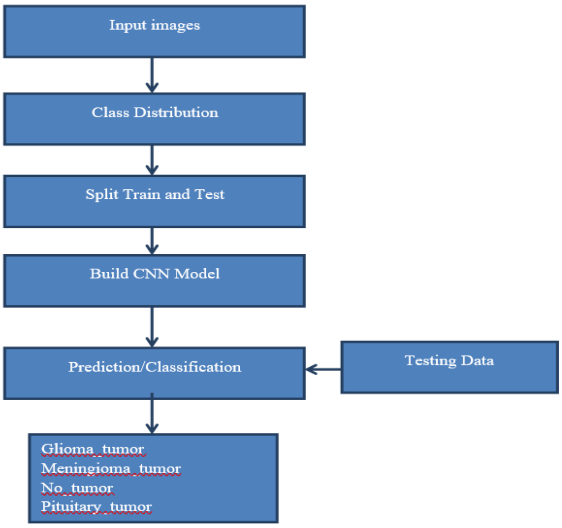


Figure 3: Data Flow Diagram

Module Design

Class Distribution

In order to make a dataset compatible with the system, some steps need to be followed. So, we had to import necessary libraries, initialize directory, resize all the images in our dataset before extracting features, standardize the data and assign different classes to different categories of tumor. These are the steps that we followed for class distribution for our entire dataset.

Extracting Features

After we used the Average pooling layer of CNN to identify unique features from all the images in our dataset and these features were used to train the CNN.

Efficient Net Learning

After extracting features from all the images in our dataset, we started building the Efficient Net Learning model. We used Efficient Net Learning version 2 for our Efficient Net Learning model and used imagenet as weights. We will keep the extracted features from the 4 classes of our dataset in the in the last layer of the pre-trained Efficient Net Learning model to get better prediction accuracy.

Training CNN

After finalizing required models, we proceeded to train the CNN (Convolutional Neural Network). We fed the features to CNN which were extracted using Efficient Net Learning model. We tried different epochs for training but the final epoch and batch size we used Batch size = 32, Image height = 224, Image weight = 224, Number of classes =4, Epochs = 30.

Save Model

We saved our model after the training was done and then started working. We saved our training code as 20f- predicts in our local directory.

Uploading Images

After deploying the model, we collected some test images to see if our model is predicting right or not. Then we started uploading images into our application and started analyzing the output.

Analyzing Outputs

After uploading an image, we have to click a button named predict and the application showed us the classification that was predicted from the uploaded image. After getting the output, we had to analyze if the prediction was correct or not, the percentage of the given prediction.

3. Result and Discussion

The implementation phase focuses how the engineer attempts to develop the system. It also deals with how data are to be structured, how procedural details are to be implemented, how interfaces are characterized, how the design will be translated into programming and hoe the testing will be performed. The methods applied during the development phase will vary but three specific technical tasks should always occur.

- The software design
- Code generation
- Software testing

The system group has changed with responsibility to develop a new system to meet requirements and design and development of new information system. The source of these study facts is variety of users at all level throughout the organization.

Stage of Development of a System

- Feasibility assessment
- Requirement analysis
- External assessment
- Architectural design
- Detailed design
- Coding
- Debugging
- Maintenance

Feasibility Assessment

In Feasibility this stage problem was defined. Criteria for choosing solution were developed, proposed possible solution, estimated costs and benefits of the system and recommended the course of action to be taken.

Requirement Analysis

During requirement analysis high-level requirement like the capabilities of the system must provide in order to solve a problem. Function requirements, performance requirements for the hardware specified during the initial planning were elaborated and made more specific in order to characterize features and the proposed system will incorporate.

External Design

External design of any software development involves conceiving, planning out and specifying the externally observable characteristic of the software product. These characteristics include user displays, report formats, external data source and data links and the functional characteristics.

Internal Design Architectural and Detailed Design

Internal design involved conceiving, planning out and specifying the internal structure and processing details in order to record the design decisions and to be able to indicate why certain alternations were chosen in preference to others. These phases also include elaboration of the test plans and provide blue prints of implementation, testing and maintenance activities. The product of internal design is architectural structure specification.

The work products of internal design are architectural structure specification, the details of the algorithm, data structure and test plan. In architectural design the conceptual view is refined.

Detailed Design

Detailed design involved specifying the algorithmic details concerned with data representation, interconnections among data structures and packaging of the software product. This phase emphasizes more on semantic issues and less synthetic details.

Coding

This phase involves actual programming, i.e, transacting detailed design into source code using appropriate programming language.

Debugging

This stage was related with removing errors from programs and making them completely error free.

Maintenance

During this stage the systems are loaded and put into use. They also get modified accordingly to the requirements of the user. These modifications included making enhancements to system and removing problems.

4. Conclusion and Future Enhancement

In this study, a novel CNN architecture with Efficient Net for classifying brain tumors was introduced. An MRI image database that is T1-weighted and contrast-enhanced that comprises the tumor classifications Glioma tumor, Meningioma tumor, No tumor, and Pituitary tumor was used to accomplish the classification. We utilized complete pictures as input, therefore no preprocessing or tumor segmentation was required. Our neural network can be operated on standard, contemporary personal computers and is less complicated than pre-trained networks. Because the algorithm uses significantly fewer resources for implementation and training, this is feasible. Underdeveloped smaller networks is also important because it may be possible to implement the algorithm on mobile platforms, which is important for diagnostics in underdeveloped nations. The ability to generalize entails making predictions for people from which we have no observations in clinical diagnostics. In light of this, the test set cannot contain the observations made by members of the training set. If this requirement is not satisfied, the confounding dependency between a patient's identity and diagnosis may cause complicated predictors to have unreasonably high prediction accuracy. We have committed to subject-wise cross-validation in light of that knowledge. As far as we are aware, no study in the literature has demonstrated tested generalization for this image database using the subject-wise k-fold approach. We achieved an accuracy of 88.48% for the enhanced dataset using the subject-wise technique. Less than

15 ms per image was the average test execution time. These results show that our network has a good generalization capability and good execution speed, so it could be used as an effective decision-support tool for radiologists in medical diagnostics.

Scope for Future Enhancement

Moreover, in the near future we want to work with a bigger dataset for example: a dataset of 1000 images using this model

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